

Attorney Docket No: 23540-07445/US

Client Ref: 2001-072-2

USSN: 09/955,663

**AMENDMENTS TO THE CLAIMS****1. (Canceled)**

**2. (Currently amended):** The method of claim 1, A method for estimating the precision of measurements taken from an array, comprising:

- (a) identifying a set of low-level data measurements;
- (b) estimating a standard deviation,  $\sigma_\epsilon$ , of an additive error component,  $\epsilon$ ;
- (c) estimating a background parameter,  $\alpha$ ;
- (d) identifying a set of replicated high-level data measurements;
- (e) estimating a standard deviation,  $\sigma_\eta$ , of a proportional error component,  $\eta$

from the standard deviation of the logarithm of the replicated high-level data set;

(f) measuring a signal,  $y$ , wherein said signal indicates an amount of a biological molecule; and

- (g) estimating a variance of the measured signal as

$$\text{Var}\{y\} = \mu^2 e^{\sigma_\eta^2} (e^{\sigma_\eta^2} - 1) + \sigma_\epsilon^2$$

wherein  $\mu$  is the amount of the biological molecule and

$$y = \alpha + \mu e^\eta + \epsilon$$

and wherein said identifying step (a) comprises the use of a thresholding algorithm to establish a cutoff, and the set of low-level data consists of those data with values less than the cutoff.

**3. (Previously amended):** The method of claim 2, wherein the thresholding algorithm comprises the steps of:

- (a) identifying  $A_N$ , an initial set of low-level data measurements consisting of  $q$  percent of the total number of data points having the lowest measurement values,  $A_N = \{x_1, x_2, \dots, x_{no}\}$ ;
- (b) calculating a mean and a standard deviation of the initial set;
- (c) calculating a cutoff point,  $u_N$  = mean plus ( $c \times$  the standard deviation),  
wherein  $2 \leq c \leq 3$ ;
- (d) defining a new set,  $A_{N+1} = \{x_j < u_N\}$ ;
- (e) calculating a mean and standard deviation of the new set; and

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(f) repeating steps (c) and (d) using the mean and standard deviation of the new set until the algorithm converges.

4. (Previously amended): The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a) identifying  $A_N$ , an initial set, of low-level data consisting of  $q$  percent of the total number of data points having the lowest measurement values,  $A_N = \{x_1, x_2, \dots, x_{n_0}\}$ ;

(b) calculating a median of the initial set,  $m_0 = \text{median } \{x_j\}_{j=1}^{n_0}$  and a median of the absolute deviations about the median,  $MAD_0 = \text{median } \{|x_j - m_0|\}_{j=1}^{n_0}$ ;

(c) calculating a cutoff point,  $u_0 = MAD_0 + (c \times s_0)$ , wherein  $s_0 = MAD_0/0.675$  and  $2 \leq c \leq 3$ ;

(d) defining a new set,  $A_{N+1} = \{x_j < u_N\}$ ;

(e) calculating a median and a median of the absolute deviations about the median of the new set; and

(f) repeating steps (c) and (d) using the median and the median of the absolute deviations about the median of the new set until the algorithm converges.

5. (Original): The method of claim 2, wherein the mean of the low-level data measurements is used as the estimate of the background parameter,  $\alpha$ .

6. (Currently amended): The method of claim 2 claim 1, wherein the standard deviation of the low-level data measurements is used as the estimate of the parameter  $\sigma_e$ .

7. (Currently amended): The method of claim 2 claim 1, wherein a mean of negative control data is used as the estimate of the background parameter,  $\alpha$ .

8. (Currently amended): The method of claim 2 claim 1, wherein the biological molecule is a nucleic acid.

9. (Original): The method of claim 8, wherein the nucleic acid is mRNA.

10. (Original): The method of claim 8, wherein the biological molecule is DNA.

11. (Original): The method of claim 10, wherein the DNA is cDNA.

12. (Original): The method of claim 10, wherein the DNA is genomic.

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13. (Canceled)

14. (Canceled)